

Sequence Listing

<110> Sang-Seok KOH
Qing LIU
Hyun-Ho CHUNG
Wen ZENG
Bog-Man LEE
Si-Young SONG

<120> GENE FAMILIES ASSOCIATED WITH LIVER CANCER

<130> 1599-0275PUS1

<140> US 10/524,530

<141> 2005-02-11

<150> US 60/402,905

<151> 2002-08-14

<150> US 60/403,651

<151> 2002-08-16

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<170> KopatentIn 1.71

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<211> 578

<212> DNA

<213> Homo sapiens

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<222> (155)..(418)

<223> Gene LBFL302, Clone BC4

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accggattgt tttcgtggc ccagtgtccc cggagcttgt gtgcgataca gagagcacct 120

cggaagctga ggcagctggt acttgacaga gagg atg gcg ctg tcg acc 169
Met Ala Leu Ser Thr
1 5

ata gtc tcc cag agg aag cag ata aag cgg aag gct ccc cgt ggc ttt 217
Ile Val Ser Gln Arg Lys Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe
10 15 20

cta aag cga gtc ttc aag cga aag aag cct caa ctt cgt ctg gag aaa 265
Leu Lys Arg Val Phe Lys Arg Lys Lys Pro Gln Leu Arg Leu Glu Lys
25 30 35

agt ggt gac tta ttg gtc cat ctg aac tgt tta ctg ttt gtt cat cga 313
Ser Gly Asp Leu Leu Val His Leu Asn Cys Leu Leu Phe Val His Arg
40 45 50

tta gca gaa gag tcc agg aca aac gct tgt gcg agt aaa tgt aga gtc 361
 Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala Ser Lys Cys Arg Val
 55 60 65
 att aac aag gag cat gta ctg gcc gca gca aag gta att cta aag aag 409
 Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys Val Ile Leu Lys Lys
 70 75 80 85
 agc aga ggt ta gaagtcaaag aacatattct tgaaagttat gatgcattct 460
 Ser Arg Gly
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 35 40 45
 Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala
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 Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys
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 Val Ile Leu Lys Lys Ser Arg Gly
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tggtacttga cagagagg .atg gcg ctg tcg acc ata gtc tcc cag agg aag	171
Met Ala Leu Ser Thr Ile Val Ser Gln Arg Lys	
1 5 10	
cag ata aag cgg aag gct ccc cgt ggc ttt cta aag cga gtc ttc aag	219
Gln Ile Lys Arg Lys Ala Pro Arg Gly Phe Leu Lys Arg Val Phe Lys	
15 20 25	
cta aag aag cct caa ctt cgt ctg gag aaa agt ggt gac tta ttg gtc	267
Leu Lys Lys Pro Gln Leu Arg Leu Glu Lys Ser Gly Asp Leu Leu Val	
30 35 40	
cat ctg aac tgt tta ctg ttt gtt cat cga tta gca gaa gag tcc agg	315
His Leu Asn Cys Leu Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg	
45 50 55	
aca aac gct tgt gcg agt aaa tgt aga gtc att aac aag gag cat gta	363
Thr Asn Ala Cys Ala Ser Lys Cys Arg Val Ile Asn Lys Glu His Val	
60 65 70 75	
ctg gcc gca gca aag gta att cta aag aag agc aga ggt tagaagtc	410
Leu Ala Ala Ala Lys Val Ile Leu Lys Lys Ser Arg Gly	
80 85	
aaagaacata ttcttgaaag ttatgatgca ttcttttggg tggtaacaga tcataaagac	470
attttttaca catcagttaa tatgggatta ttaaattattg gatataaaaaa aaaaaaaaaa	530
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35 40 45
Leu Phe Val His Arg Leu Ala Glu Glu Ser Arg Thr Asn Ala Cys Ala
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Ser Lys Cys Arg Val Ile Asn Lys Glu His Val Leu Ala Ala Ala Lys
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Val Ile Leu Lys Lys Ser Arg Gly
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Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys Pro Gly Glu Leu Gly
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ctt cct cac ccc ctc agc aca gga gga ctc cct gta gcc tca gaa gat          142
Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro Val Ala Ser Glu Asp
              25              30              35

gga gct ctc agg gcc cct gag agc caa agc gtg acc ccc aag cca ctg          190
Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val Thr Pro Lys Pro Leu
              40              45              50

gag act gag cct agc agg gag acc gcc tgg tcc ata ggc ctt cag gtg          238
Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser Ile Gly Leu Gln Val
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acc gtg ccc ttc atg ttt gca ggc ctg gga ctg tcc tgg gcc ggc atg          286
Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu Ser Trp Ala Gly Met
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ctt ctg gac tat ttc cag gcc aac act gga caa att gat gac ccc cag          334
Leu Leu Asp Tyr Phe Gln Ala Asn Thr Gly Gln Ile Asp Asp Pro Gln
              90              95              100

gag cag cac aga gtc atc agc agc aac ctg gcc ctc atc cag gtg cag          382
Glu Gln His Arg Val Ile Ser Ser Asn Leu Ala Leu Ile Gln Val Gln
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gcc act gtc gtg ggg ctc ttg gct gct gtg gct gcg ctg ctg ttg ggc          430
Ala Thr Val Val Gly Leu Leu Ala Ala Val Ala Ala Leu Leu Leu Gly
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gtg gtg tct cga gag gaa gtg gat gtc gcc aag gtg gag ttg ctg tgt          478
Val Val Ser Arg Glu Glu Val Asp Val Ala Lys Val Glu Leu Leu Cys
              135              140              145

gcc agc agt gtc ctc act gcc ttc ctt gca gcc ttt gcc ctg ggg gtg          526
Ala Ser Ser Val Leu Thr Ala Phe Leu Ala Ala Phe Ala Leu Gly Val
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ctg atg gtc tgt ata gtg att ggt gct cga aag ctc ggg gtc aac cca          574

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Leu Ser Ile Leu Ala Leu Val Ser Ser Phe Phe Tyr Arg His Lys Asp	
200 205 210	
agt cgg tat ctg acg ccg ctg gtc tgc ctc agc ttt gcg gct ctg acc	718
Ser Arg Tyr Leu Thr Pro Leu Val Cys Leu Ser Phe Ala Ala Leu Thr	
215 220 225	
cca gtg tgg gtc ctc att gcc aag cag agc cca ccc atc gtg aag atc	766
Pro Val Trp Val Leu Ile Ala Lys Gln Ser Pro Pro Ile Val Lys Ile	
230 235 240 245	
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Leu Lys Phe Gly Trp Phe Pro Ile Ile Leu Ala Met Val Ile Ser Ser	
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ttc gga gga ctc atc ttg agc aaa acc gtt tct aaa cag cag tac aaa	862
Phe Gly Gly Leu Ile Leu Ser Lys Thr Val Ser Lys Gln Gln Tyr Lys	
265 270 275	
ggc atg gcg ata ttt acc ccc gtc ata tgt ggt gtt ggt ggc aat ctg	910
Gly Met Ala Ile Phe Thr Pro Val Ile Cys Gly Val Gly Gly Asn Leu	
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gtg gcc att cag acc agc cga atc tca acc tac ctg cac atg tgg agt	958
Val Ala Ile Gln Thr Ser Arg Ile Ser Thr Tyr Leu His Met Trp Ser	
295 300 305	
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Ala Pro Gly Val Leu Pro Leu Gln Met Lys Lys Phe Trp Pro Asn Pro	
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Leu Leu Leu Leu Val Val Pro Gly His Leu Ile Phe Phe Tyr Ile Ile	
345 350 355	
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Tyr Leu Val Glu Gly Gln Ser Val Ile Asn Ser Gln Thr Phe Val Val	
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ctc tac ctg ctg gca ggc ctg atc cag gtg aca atc ctg ctg tac ctg	1198
Leu Tyr Leu Leu Ala Gly Leu Ile Gln Val Thr Ile Leu Leu Tyr Leu	
375 380 385	
gca gaa gtg atg gtt cgg ctg act tgg cac cag gcc ctg gat cct gac	1246
Ala Glu Val Met Val Arg Leu Thr Trp His Gln Ala Leu Asp Pro Asp	

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aac cac tgc atc ccc tac ctt aca ggg ctg ggg gac ctg ctc ggt act				1294
Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly Asp Leu Leu Gly Thr				
	410	415	420	
ggc ctc ctg gca ctc tgc ttt ttc act gac tgg cta ctg aag agc aag				1342
Gly Leu Leu Ala Leu Cys Phe Phe Thr Asp Trp Leu Leu Lys Ser Lys				
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gca gag ctg ggt ggc atc tca gaa ctg gca tct gga cct ccc taactg				1390
Ala Glu Leu Gly Gly Ile Ser Glu Leu Ala Ser Gly Pro Pro				
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 35 40 45
 Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
 50 55 60

Ile	Gly	Leu	Gln	Val	Thr	Val	Pro	Phe	Met	Phe	Ala	Gly	Leu	Gly	Leu		65	70	75	80
Ser	Trp	Ala	Gly	Met	Leu	Leu	Asp	Tyr	Phe	Gln	Ala	Asn	Thr	Gly	Gln		85	90	95	
Ile	Asp	Asp	Pro	Gln	Glu	Gln	His	Arg	Val	Ile	Ser	Ser	Asn	Leu	Ala		100	105	110	
Leu	Ile	Gln	Val	Gln	Ala	Thr	Val	Val	Gly	Leu	Leu	Ala	Ala	Val	Ala		115	120	125	
Ala	Leu	Leu	Leu	Gly	Val	Val	Ser	Arg	Glu	Glu	Val	Asp	Val	Ala	Lys		130	135	140	
Val	Glu	Leu	Leu	Cys	Ala	Ser	Ser	Val	Leu	Thr	Ala	Phe	Leu	Ala	Ala		145	150	155	160
Phe	Ala	Leu	Gly	Val	Leu	Met	Val	Cys	Ile	Val	Ile	Gly	Ala	Arg	Lys		165	170	175	
Leu	Gly	Val	Asn	Pro	Asp	Asn	Ile	Ala	Thr	Pro	Ile	Ala	Ala	Ser	Leu		180	185	190	
Gly	Asp	Leu	Ile	Thr	Leu	Ser	Ile	Leu	Ala	Leu	Val	Ser	Ser	Phe	Phe		195	200	205	
Tyr	Arg	His	Lys	Asp	Ser	Arg	Tyr	Leu	Thr	Pro	Leu	Val	Cys	Leu	Ser		210	215	220	
Phe	Ala	Ala	Leu	Thr	Pro	Val	Trp	Val	Leu	Ile	Ala	Lys	Gln	Ser	Pro		225	230	235	240
Pro	Ile	Val	Lys	Ile	Leu	Lys	Phe	Gly	Trp	Phe	Pro	Ile	Ile	Leu	Ala		245	250	255	
Met	Val	Ile	Ser	Ser	Phe	Gly	Gly	Leu	Ile	Leu	Ser	Lys	Thr	Val	Ser		260	265	270	
Lys	Gln	Gln	Tyr	Lys	Gly	Met	Ala	Ile	Phe	Thr	Pro	Val	Ile	Cys	Gly		275	280	285	
Val	Gly	Gly	Asn	Leu	Val	Ala	Ile	Gln	Thr	Ser	Arg	Ile	Ser	Thr	Tyr		290	295	300	
Leu	His	Met	Trp	Ser	Ala	Pro	Gly	Val	Leu	Pro	Leu	Gln	Met	Lys	Lys		305	310	315	320
Phe	Trp	Pro	Asn	Pro	Cys	Ser	Thr	Phe	Cys	Thr	Ser	Glu	Ile	Asn	Ser		325	330	335	
Met	Ser	Ala	Arg	Val	Leu	Leu	Leu	Leu	Val	Val	Pro	Gly	His	Leu	Ile		340	345	350	
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Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu Ile Gln Val Thr
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Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu Thr Trp His Gln
 385 390 395 400

Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly
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Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe Phe Thr Asp Trp
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 <223> Clone MB5

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 Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val Thr Pro Lys Pro Leu
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 Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser Ile Gly Leu Gln Val
 55 60 65

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 Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu Ser Trp Ala Gly Met
 70 75 80 85

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			120				125					130								
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230					235				240						245					
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Ile	Val	Lys	Ile	Leu	Lys	Phe	Gly	Trp	Phe	Pro	Ile	Ile	Leu	Ala	Met					
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310					315					320					325					

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tca gct cga gtc ctg ctc ttg ctg gtg gtc cca ggc cat ctg att ttc Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro Gly His Leu Ile Phe 375 380 385	1207
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gccacactgc tgctgtgcca agaaggtgta cagcctcccc aggatggggc ctcatacaac 2030
 ccttcacatc cactcaacat ttaatcgtgt ccttgctgtc tttttatattt cctttttgtt 2090
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 <211> 487
 <212> PRT
 <213> Homo sapiens

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 Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
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 Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
 35 40 45
 Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
 50 55 60
 Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
 65 70 75 80
 Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe
 85 90 95
 Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu
 100 105 110
 Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala
 115 120 125
 Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser
 130 135 140
 Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu
 145 150 155 160
 Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val
 165 170 175
 Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala
 180 185 190
 Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile
 195 200 205
 Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile
 210 215 220

Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val
 225 230 235 240
 Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu
 245 250 255
 Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala
 260 265 270
 Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro
 275 280 285
 Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser
 290 295 300
 Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro
 305 310 315 320
 Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg
 325 330 335
 Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu
 340 345 350
 Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser
 355 360 365
 Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro
 370 375 380
 Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser
 385 390 395 400
 Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu
 405 410 415
 Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu
 420 425 430
 Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
 435 440 445
 Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe
 450 455 460
 Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser
 465 470 475 480
 Glu Leu Ala Ser Gly Pro Pro
 485

<210> 9
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 <212> DNA
 <213> Homo sapiens

[illegible]

Cys	Ala	Ser	Ser	Val	Leu	Thr	Ala	Phe	Leu	Ala	Ala	Phe	Ala	Leu	Gly	
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gtg	ctg	atg	gtc	tgt	ata	gtg	att	ggg	gct	cga	aag	ctc	ggg	gtc	aac	678
Val	Leu	Met	Val	Cys	Ile	Val	Ile	Gly	Ala	Arg	Lys	Leu	Gly	Val	Asn	
				205					210					215		
cca	gac	aac	att	gcc	acg	ccc	att	gca	gcc	agc	ctg	gga	gac	ctc	atc	726
Pro	Asp	Asn	Ile	Ala	Thr	Pro	Ile	Ala	Ala	Ser	Leu	Gly	Asp	Leu	Ile	
			220					225					230			
aca	ctg	tcc	att	ctg	gct	ttg	gtt	agc	agc	ttc	ttc	tac	aga	cac	aaa	774
Thr	Leu	Ser	Ile	Leu	Ala	Leu	Val	Ser	Ser	Phe	Phe	Tyr	Arg	His	Lys	
		235					240					245				
gat	agt	cgg	tat	ctg	acg	ccg	ctg	gtc	tgc	ctc	agc	ttt	gcg	gct	ctg	822
Asp	Ser	Arg	Tyr	Leu	Thr	Pro	Leu	Val	Cys	Leu	Ser	Phe	Ala	Ala	Leu	
	250					255					260					
acc	cca	gtg	tgg	gtc	ctc	att	gcc	aag	cag	agc	cca	ccc	atc	gtg	aag	870
Thr	Pro	Val	Trp	Val	Leu	Ile	Ala	Lys	Gln	Ser	Pro	Pro	Ile	Val	Lys	
265					270					275					280	
atc	ctg	aag	ttt	ggc	tgg	ttc	cca	atc	atc	ctg	gcc	atg	gtc	atc	agc	918
Ile	Leu	Lys	Phe	Gly	Trp	Phe	Pro	Ile	Ile	Leu	Ala	Met	Val	Ile	Ser	
				285					290					295		
agt	ttc	gga	gga	ctc	atc	ttg	agc	aaa	acc	gtt	tct	aaa	cag	cag	tac	966
Ser	Phe	Gly	Gly	Leu	Ile	Leu	Ser	Lys	Thr	Val	Ser	Lys	Gln	Gln	Tyr	
			300					305					310			
aaa	ggc	atg	gcg	ata	ttt	acc	ccc	gtc	ata	tgt	ggg	gtt	ggg	ggc	aat	1014
Lys	Gly	Met	Ala	Ile	Phe	Thr	Pro	Val	Ile	Cys	Gly	Val	Gly	Gly	Asn	
		315					320					325				
ctg	gtg	gcc	att	cag	acc	agc	cga	atc	tca	acc	tac	ctg	cac	atg	tgg	1062
Leu	Val	Ala	Ile	Gln	Thr	Ser	Arg	Ile	Ser	Thr	Tyr	Leu	His	Met	Trp	
		330					335					340				
agt	gca	cct	ggc	gtc	ctg	ccc	ctc	cag	atg	aag	aaa	ttc	tgg	ccc	aac	1110
Ser	Ala	Pro	Gly	Val	Leu	Pro	Leu	Gln	Met	Lys	Lys	Phe	Trp	Pro	Asn	
345					350					355					360	
ccg	tgt	tct	act	ttc	tgc	acg	tca	gaa	atc	aat	tcc	atg	tca	gct	cga	1158
Pro	Cys	Ser	Thr	Phe	Cys	Thr	Ser	Glu	Ile	Asn	Ser	Met	Ser	Ala	Arg	
				365					370					375		
gtc	ctg	ctc	ttg	ctg	gtg	gtc	cca	ggc	cat	ctg	att	ttc	ttc	tac	atc	1206
Val	Leu	Leu	Leu	Leu	Val	Val	Pro	Gly	His	Leu	Ile	Phe	Phe	Tyr	Ile	
			380					385					390			
atc	tac	ctg	gtg	gag	ggg	cag	tca	gtc	ata	aac	agc	cag	acc	ttt	gtg	1254
Ile	Tyr	Leu	Val	Glu	Gly	Gln	Ser	Val	Ile	Asn	Ser	Gln	Thr	Phe	Val	
		395					400					405				
gtg	ctc	tac	ctg	ctg	gca	ggc	ctg	atc	cag	gtg	aca	atc	ctg	ctg	tac	1302
Val	Leu	Tyr	Leu	Leu	Ala	Gly	Leu	Ile	Gln	Val	Thr	Ile	Leu	Leu	Tyr	

410	415	420	
ctg gca gaa gtg atg gtt cgg ctg act tgg cac cag gcc ctg gat cct			1350
Leu Ala Glu Val Met Val Arg Leu Thr Trp His Gln Ala Leu Asp Pro			
425	430	435	440
gac aac cac tgc atc ccc tac ctt aca ggg ctg ggg gac ctg ctc ggt			1398
Asp Asn His Cys Ile Pro Tyr Leu Thr Gly Leu Gly Asp Leu Leu Gly			
	445	450	455
tca agc tcc gtg ggc cac act gct gct gtg cca aga agg tgt aca gcc			1446
Ser Ser Ser Val Gly His Thr Ala Ala Val Pro Arg Arg Cys Thr Ala			
	460	465	470
tcc cca gga tgg ggc ctc ata caa ccc ttc atc tgc act caa cat tta			1494
Ser Pro Gly Trp Gly Leu Ile Gln Pro Phe Ile Cys Thr Gln His Leu			
	475	480	485
atc gtg tcc ttg ctg tct ttt tat ttt cct ttt tgt ttg tta gca aaa			1542
Ile Val Ser Leu Leu Ser Phe Tyr Phe Pro Phe Cys Leu Leu Ala Lys			
	490	495	500
acc tct att tagatttca ataatcagag aagtgtaaaa taaaacagat tatattgtaa			1600
Thr Ser Ile			
505			
aaaaaaaaaa aaaaaa			1616

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 <213> Homo sapiens

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 Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys
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 Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
 20 25 30
 Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
 35 40 45
 Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
 50 55 60
 Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
 65 70 75 80
 Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe
 85 90 95
 Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu
 100 105 110
 Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala

115					120					125					
Asn	Thr	Gly	Gln	Ile	Asp	Asp	Pro	Gln	Glu	Gln	His	Arg	Val	Ile	Ser
130					135					140					
Ser	Asn	Leu	Ala	Leu	Ile	Gln	Val	Gln	Ala	Thr	Val	Val	Gly	Leu	Leu
145					150					155					160
Ala	Ala	Val	Ala	Ala	Leu	Leu	Leu	Gly	Val	Val	Ser	Arg	Glu	Glu	Val
					165					170					175
Asp	Val	Ala	Lys	Val	Glu	Leu	Leu	Cys	Ala	Ser	Ser	Val	Leu	Thr	Ala
					180					185					190
Phe	Leu	Ala	Ala	Phe	Ala	Leu	Gly	Val	Leu	Met	Val	Cys	Ile	Val	Ile
					195					200					205
Gly	Ala	Arg	Lys	Leu	Gly	Val	Asn	Pro	Asp	Asn	Ile	Ala	Thr	Pro	Ile
					210					215					220
Ala	Ala	Ser	Leu	Gly	Asp	Leu	Ile	Thr	Leu	Ser	Ile	Leu	Ala	Leu	Val
225					230					235					240
Ser	Ser	Phe	Phe	Tyr	Arg	His	Lys	Asp	Ser	Arg	Tyr	Leu	Thr	Pro	Leu
					245					250					255
Val	Cys	Leu	Ser	Phe	Ala	Ala	Leu	Thr	Pro	Val	Trp	Val	Leu	Ile	Ala
					260					265					270
Lys	Gln	Ser	Pro	Pro	Ile	Val	Lys	Ile	Leu	Lys	Phe	Gly	Trp	Phe	Pro
					275					280					285
Ile	Ile	Leu	Ala	Met	Val	Ile	Ser	Ser	Phe	Gly	Gly	Leu	Ile	Leu	Ser
					290					295					300
Lys	Thr	Val	Ser	Lys	Gln	Gln	Tyr	Lys	Gly	Met	Ala	Ile	Phe	Thr	Pro
305					310					315					320
Val	Ile	Cys	Gly	Val	Gly	Gly	Asn	Leu	Val	Ala	Ile	Gln	Thr	Ser	Arg
					325					330					335
Ile	Ser	Thr	Tyr	Leu	His	Met	Trp	Ser	Ala	Pro	Gly	Val	Leu	Pro	Leu
					340					345					350
Gln	Met	Lys	Lys	Phe	Trp	Pro	Asn	Pro	Cys	Ser	Thr	Phe	Cys	Thr	Ser
					355					360					365
Glu	Ile	Asn	Ser	Met	Ser	Ala	Arg	Val	Leu	Leu	Leu	Leu	Val	Val	Pro
					370					375					380
Gly	His	Leu	Ile	Phe	Phe	Tyr	Ile	Ile	Tyr	Leu	Val	Glu	Gly	Gln	Ser
385					390					395					400
Val	Ile	Asn	Ser	Gln	Thr	Phe	Val	Val	Leu	Tyr	Leu	Leu	Ala	Gly	Leu
					405					410					415
Ile	Gln	Val	Thr	Ile	Leu	Leu	Tyr	Leu	Ala	Glu	Val	Met	Val	Arg	Leu

	420		425		430
Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu					
435		440		445	
Thr Gly Leu Gly Asp Leu Leu Gly Ser Ser Ser Val Gly His Thr Ala					
450		455		460	
Ala Val Pro Arg Arg Cys Thr Ala Ser Pro Gly Trp Gly Leu Ile Gln					
465		470		475	480
Pro Phe Ile Cys Thr Gln His Leu Ile Val Ser Leu Leu Ser Phe Tyr					
	485		490		495
Phe Pro Phe Cys Leu Leu Ala Lys Thr Ser Ile					
500		505			